SUPPORT FOR THE AMENDMENTS

Claims 1-19 have been canceled.

Claims 20-37 have been added.

New Claims 20-37 are supported by the claims and the specification as originally filed at page 3, line 7 to page 59, line 10.

The specification has been amended in accordance with the Examiner's requirement to correct grammatical errors and use of improper idiomatic English.

No new matter has been entered by the present amendment.

REMARKS

Claims 20-37 are active in the present application.

The rejections of Claim 12 under 35 U.S.C. §102(b) over Baggio et al and Teller et al are obviated by amendment. Claims 1-19 have been canceled and Claims 20-37 have been introduced in place thereof.

Baggio et al and Teller et al disclose glutamate dehydrogenase sequences which comprise the sequences TTGACA at position –63 (see alignment provided in Paper No. 10 regarding Baggio et al) or TATAAT at position –168 (see alignment provided in Paper No. 10 regarding Teller et al). Neither of these references disclose or suggest the glutamic acid synthesizing gene having the claimed sequences at position –35 or at –10 in the promoter region.

The standard for determining anticipation requires that the reference "must teach every element of the claim" (MPEP §2131). For the reasons set forth above, Baggio et al and Teller et al fail to meet this standard. Therefore, the rejections over Baggio et al and Teller et al are no longer tenable.

Applicants request withdrawal of these grounds of rejection.

The rejections of Claims 12 and 14 under 35 U.S.C. §112, first paragraph (written description and enablement), are obviated by amendment.

In making the written description rejection, the Examiner concedes that the specification adequately discloses the production of coryneform bacteria having mutant promoters for the coryneform bacteria glutamate dehydrogenase, citrate synthase, isocitrate synthase, pyruvate dehydrogenase, and aconitase genes (paper number 16, page 7, line 23 to

page 8, line 2). Consistent with this indication, Applicants have canceled original Claims 1-19 and replaced them with new Claims 20-37. Claim 20 provides:

> A glutamic acid synthesizing gene *selected from the group consisting of glutamate dehydrogenase, citrate synthase, isocitrate synthase, pyruvate dehydrogenase, and aconitase*, comprising a DNA sequence situated at position -35 in a promoter sequence of the glutamic acid synthesizing gene, wherein said DNA sequence is selected from the group consisting of CGGTCA, TTGTCA, TTGACA, and TTGCCA. (*emphasis added*)

Therefore, as recognized by the Examiner and set forth above, new Claim 20 (and the claims dependent therefrom) satisfies the threshold written description requirements of 35 U.S.C. §112, first paragraph.

The Examiner also rejected original Claims 12 and 14 for lack of enablement. However, it is noted that the Examiner recognizes the enablement of coryneform bacterium glutamate dehydrogenase gene linked to a mutated coryneform bacterium promoter comprising the hexamers as recited in previous Claim 4 (see paper number 16, page 9, lines 5-7). Consistent with this indication, Claim 20 now includes a specification recitation that the glutamic acid synthesizing gene comprises a DNA sequence situated at position -35 in a promoter sequence of the glutamic acid synthesizing gene, wherein said DNA sequence is selected from the group consisting of CGGTCA, TTGTCA, TTGACA, and TTGCCA (see Claim 20). As such, Claim 20 (and the claims dependent therefrom) is fully enabled.

Withdrawal of these grounds of rejection is requested.

The rejection of Claims 12 and 14 under 35 U.S.C. §112, second paragraph, is obviated by amendment.

Applicants note that Claims 12 and 14 have been canceled, along with the remainder of Claims 1-19, and replace with new Claims 20-37. Applicants submit new Claims 20-37 are free from the criticisms set forth by the Examiner in relation to Claims 12 and 14.

Specifically, Applicants have removed the dependency from Claim 4 and the alleged lack of antecedent basis. In addition, Applicants have defined the objected to term "glutamic acid-synthesizing gene" as being "selected from the group consisting of glutamate dehydrogenase, citrate synthase, isocitrate synthase, pyruvate dehydrogenase, and aconitase" (see Claim 20). Further, consistent with the Examiner's suggestion, Applicants have defined the DNA sequence situated at position -35 in a promoter sequence of the glutamic acid synthesizing gene, wherein said DNA sequence is selected from the group consisting of CGGTCA, TTGTCA, TTGACA, and TTGCCA (see Claim 20).

Accordingly, Applicants request withdrawal of this ground of rejection.

The objection of Claim 12 as being dependent upon non-elected Claim 4 is obviated by the cancellation of Claims 1-19. It is requested that the Examiner acknowledge the same in the next communication from the Office.

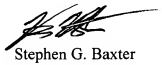
The objection to the Abstract is believed to be obviated by the submission of a substitute Abstract incorporating the amendments that the Examiner has kindly suggested. In addition, the objection to the disclosure is also believed to be obviated by amendment.

Applicants request withdrawal of these grounds of objection.

Applicants submit that the present application is in condition for allowance. Early notification to this effect is respectfully requested.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.



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